



SEQUENCE LISTING

<110> Bates, Elizabeth
Fournier, Nathalie
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Garrone, Pierre

<120> MONOCYTE-DERIVED NUCLEIC ACIDS AND RELATED COMPOSITIONS AND METHODS

<130> SF0977XB

<140> US 10/780,043
<141> 2004-02-17

<150> US 09/869,388
<151> 1999-12-29

<150> US 09/223,919
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Tyr	Tyr	Pro	Trp 40	Glu	Leu	Ala	Thr	Ala 45	Pro	Asp	Val	Arg	Ile 50	Ser	Trp		
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Ser	Ile 70	His	Lys	Asp	Tyr	Val 75	Asn	Arg	Leu	Phe	Leu 80	Asn	Trp	Thr	Glu		
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Gln	Ser	Val	Tyr	Phe 105	Cys	Arg	Val	Glu	Leu 110	Asp	Thr	Arg	Ser	Ser 115	Gly		
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Arg	Leu 150	Ser	Ser	Thr	Thr	Thr 155	Thr	Thr	Gly	Leu	Arg 160	Val	Thr	Gln	Gly		
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gtg	gca	gtg	gct	gtc	act	gtg	ctc	gga	atc	atg	att	ttg	gga	ctg	atc	798	
Val	Ala	Val	Ala	Val 185	Thr	Val	Leu	Gly	Ile 190	Met	Ile	Leu	Gly	Leu 195	Ile		
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Cys	Leu	Leu	Arg 200	Trp	Arg	Arg	Arg	Lys 205	Gly	Gln	Gln	Arg	Thr 210	Lys	Ala		
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Asn	Ile 230	Arg	Asn	Glu	Gly	Gln 235	Asn	Thr	Asp	Pro	Lys 240	Leu	Asn	Pro	Lys		
gat	gac	ggc	atc	gta	tat	gct	tcc	ctt	gcc	ctc	tcc	agc	tcc	acc	tca	990	
Asp	Asp	Gly	Ile	Val 245	Tyr 250	Ala	Ser	Leu	Ala 255	Leu	Ser	Ser	Ser	Thr	Ser 260		
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Pro	Arg	Ala	Pro	Pro 265	Ser	His	Arg	Pro	Leu 270	Lys	Ser	Pro	Gln 275	Asn	Glu		
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Thr Leu Tyr Ser Val Leu Lys Ala
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Pro Asp Val Arg Ile Ser Trp Arg Arg Gly His Phe His Gly Gln Ser
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Phe Tyr Ser Thr Arg Pro Pro Ser Ile His Lys Asp Tyr Val Asn Arg
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Ser Asn Leu Gln Lys Gln Asp Gln Ser Val Tyr Phe Cys Arg Val Glu
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Thr Lys Leu Ser Ile Thr Gln Ala Val Thr Thr Thr Thr Gln Arg Pro
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Gly Leu Arg Val Thr Gln Gly Lys Arg Arg Ser Asp Ser Trp His Ile
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cag tcc ttc tac agc aca agg ccg cct tcc att cac aag gat tat gtg Gln Ser Phe Tyr Ser Thr Arg Pro Pro Ser Ile His Lys Asp Tyr Val 65 70 75	411
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agg atc tcc aac ctg cag aag cag gac cag tct gtg tat ttc tgc cga Arg Ile Ser Asn Leu Gln Lys Gln Asp Gln Ser Val Tyr Phe Cys Arg 95 100 105	507
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 Arg Asn Glu Gly Gln Asn Thr Asp Pro Lys Leu Asn Pro Lys Asp Asp
 160 165 170 175
 Gly Ile Val Tyr Ala Ser Leu Ala Leu Ser Ser Ser Thr Ser Pro Arg
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ggccctcagg cagccctcc acagggcccc tctcctgcct ggacagctct gctggtctcc 360

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Gly Ser Gly Pro Ser Tyr Leu Tyr Gly Val Thr Gln Pro Lys His Leu
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Ser Ala Ser Met Gly Gly Ser Val Glu Ile Pro Phe Ser Phe Tyr Tyr
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Gly His Phe His Gly Gln Ser Phe Tyr Ser Thr Arg Pro Pro Ser Ile
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His Lys Asp Tyr Val Asn Arg Leu Phe Leu Asn Trp Thr Glu Gly Gln
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gag agc ggc ttc ctc agg atc tca aac ctg cgg aag gag gac cag tct 748
Glu Ser Gly Phe Leu Arg Ile Ser Asn Leu Arg Lys Glu Asp Gln Ser
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Val Tyr Phe Cys Arg Val Glu Leu Asp Thr Arg Arg Ser Gly Arg Gln
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cag ttg cag tcc atc aag ggg acc aaa ctc acc atc acc cag gct gtc 844
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Gly His Ser Glu Ser Trp His Leu Ser Leu Asp Thr Ala Ile Arg Val
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Ala Leu Ala Val Ala Val Leu Lys Thr Val Ile Leu Gly Leu Leu Cys
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Gly Ser Val Glu Ile Pro Phe Ser Phe Tyr Tyr Pro Trp Glu Leu Ala	
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Thr Ala Pro Asp Val Arg Ile Ser Trp Arg Arg Gly His Phe His Gly	
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Gln Ser Phe Tyr Ser Thr Arg Pro Pro Ser Ile His Lys Asp Tyr Val	
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Asn Arg Leu Phe Leu Asn Trp Thr Glu Gly Gln Lys Ser Gly Phe Leu	
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Arg Ile Ser Asn Leu Gln Lys Gln Asp Gln Ser Val Tyr Phe Cys Arg	
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Arg Ser His Met Arg Ile Ser Gly Met Lys Asp Lys Ile Gln Ile Pro	
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ctgtactctg tcttaaaggc ctaaccaatg gacagccctc tcaagactga atggtgaggc	824
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-10

-5

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 35 40 45
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 50 55 60
 Phe Tyr Ser Thr Arg Pro Pro Ser Ile His Lys Asp Tyr Val Asn Arg
 65 70 75
 Leu Phe Leu Asn Trp Thr Glu Gly Gln Lys Ser Gly Phe Leu Arg Ile
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 Ser Asn Leu Gln Lys Gln Asp Gln Ser Val Tyr Phe Cys Arg Val Glu
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gtc gag ctg gac acc cgg aga tca ggg agg cag cag ttg cag tcc atc Val Glu Leu Asp Thr Arg Arg Ser Gly Arg Gln Gln Leu Gln Ser Ile 130 135 140	734
aag ggg acc aaa ctc acc atc acc cag gct gtc aca acc acc acc acc Lys Gly Thr Lys Leu Thr Ile Thr Gln Ala Val Thr Thr Thr Thr 145 150 155	782
tgg agg ccc agc agc aca acc acc ata gcc ggc ctc agg gtc aca gaa Trp Arg Pro Ser Ser Thr Thr Thr Ile Ala Gly Leu Arg Val Thr Glu 160 165 170	830
agc aaa ggg cac tca gaa tca tgg cac cta agt ctg gac act gcc atc Ser Lys Gly His Ser Glu Ser Trp His Leu Ser Leu Asp Thr Ala Ile 175 180 185 190	878
agg gtt gca ttg gct gtc gct gtg ctc aaa act gtc att ttg gga ctg Arg Val Ala Leu Ala Val Ala Val Leu Lys Thr Val Ile Leu Gly Leu 195 200 205	926
ctg tgc ctc ctc ctg tgg tgg agg aga agg aaa ggt agc agg gcg cca Leu Cys Leu Leu Leu Trp Trp Arg Arg Arg Lys Gly Ser Arg Ala Pro 210 215 220	974
agc agt gac ttc tgaccaacag agtgtgggga gaagggatgt gtattagccc Ser Ser Asp Phe 225	1026

cggaggacgt gatgtgagac ccgcttgtga gtcctccaca ctcgttcccc attggcaaga 1086
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 aaaaaaaaaa aaa 1459

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 <212> PRT
 <213> Homo sapiens

<400> 10

Met Gly Arg Pro Leu Leu Leu Pro Leu Leu Leu Leu Gln Pro Pro
 1 5 10 15

Ala Phe Leu Gln Pro Gly Gly Ser Thr Gly Ser Gly Pro Ser Tyr Leu
 20 25 30

Tyr Gly Val Thr Gln Pro Lys His Leu Ser Ala Ser Met Gly Gly Ser
 35 40 45

Val Glu Ile Pro Phe Ser Phe Tyr Tyr Pro Trp Glu Leu Ala Thr Ala
 50 55 60

Pro Asp Val Arg Ile Ser Trp Arg Arg Gly His Phe His Gly Gln Ser
 65 70 75 80

Phe Tyr Ser Thr Arg Pro Pro Ser Ile His Lys Asp Tyr Val Asn Arg
 85 90 95

Leu Phe Leu Asn Trp Thr Glu Gly Gln Glu Ser Gly Phe Leu Arg Ile
 100 105 110

Ser Asn Leu Arg Lys Glu Asp Gln Ser Val Tyr Phe Cys Arg Val Glu
 115 120 125

Leu Asp Thr Arg Arg Ser Gly Arg Gln Gln Leu Gln Ser Ile Lys Gly
 130 135 140

Thr Lys Leu Thr Ile Thr Gln Ala Val Thr Thr Thr Thr Trp Arg
 145 150 155 160

Pro Ser Ser Thr Thr Thr Ile Ala Gly Leu Arg Val Thr Glu Ser Lys
165 170 175

Gly His Ser Glu Ser Trp His Leu Ser Leu Asp Thr Ala Ile Arg Val
180 185 190

Ala Leu Ala Val Ala Val Leu Lys Thr Val Ile Leu Gly Leu Leu Cys
195 200 205

Leu Leu Leu Trp Trp Arg Arg Arg Lys Gly Ser Arg Ala Pro Ser Ser
210 215 220

Asp Phe
225

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<212> DNA
<213> Homo sapiens

<400> 11
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<210> 12
<211> 21
<212> DNA
<213> Homo sapiens

<400> 12
aagctggccc tgaactcctg g 21

<210> 13
<211> 18
<212> DNA
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<400> 13
caagggataa aaaggcac 18

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<400> 14
aactctcctc cagtcggt 18

<210> 15
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<212> PRT
<213> Homo sapiens

<400> 15

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
 1 5 10 15
 Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Val Ser Ser Gly
 20 25 30
 Ser Tyr Tyr Trp Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu
 35 40 45
 Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr Asn Arg Ser
 50 55 60
 His Lys Ser Arg Val Asn Ile Ser Val Asp Thr Ala Lys Asn Gln Phe
 65 70 75 80
 Ser Leu Lys Leu Ser Ser Val Ser Thr Ala Asp Thr Ala Val Tyr Tyr
 85 90 95
 Cys Ala Arg Ile Thr Thr Thr Val Pro Ser Ser Trp Tyr Tyr Tyr Tyr
 100 105 110
 Met Asp Val Trp Asp Lys Gly Thr Thr Val Thr Val Ser Ser
 115 120 125

<210> 16
 <211> 121
 <212> PRT
 <213> Homo sapiens

<400> 16

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
 1 5 10 15
 Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Ser Ile Ser Ser Gly
 20 25 30
 Tyr Tyr Trp Gly Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp
 35 40 45
 Ile Gly Ser Ile Tyr His Ser Gly Ser Thr Tyr Tyr Asn Pro Ser Leu
 50 55 60
 Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser
 65 70 75 80
 Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Val Arg Arg Arg Tyr Ser Ser Ser Ala Ser Lys Ile Ile Phe

		100					105			110
Gly	Ser	Gly	Thr	Arg	Leu	Ser	Ile	Arg		
		115					120			